

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1605	100.0	317	8	ADH01242	Adh01242 Alpha-ket
2	595	37.1	319	7	ADC96588	Adc96588 E. faeciu
3	593.5	37.0	312	9	ADV16664	Adv16664 E. faeciu
4	593.5	37.0	326	7	ADC95776	Adc95776 E. faeciu
5	575.5	35.9	312	5	ABB54660	Abb54660 Lactococc
6	559	34.8	345	7	ADH86803	Adh86803 Enterococ
7	558.5	34.8	301	8	ADM93781	Adm93781 Enterococ
8	551.5	34.4	302	9	ADV16488	Adv16488 E. faecal
9	551	34.3	307	5	ABP28447	Abp28447 Streptoco
10	551	34.3	307	8	ADV88550	Adv88550 Streptoco
11	551	34.3	307	8	ADV81958	Adv81958 Streptoco
12	551	34.3	307	8	ADV79803	Adv79803 Streptoco
13	541	33.7	307	5	ABP28448	Abp28448 Streptoco

Database : Issued_Patents_AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	595	37.1	319	2	US-09-107-532A-6215	Sequence 6215, Ap
2	593.5	37.0	326	2	US-09-107-532A-5403	Sequence 5403, Ap
3	559	34.8	345	2	US-09-134-000C-4688	Sequence 4688, Ap
4	474	29.5	279	2	US-09-134-000C-5430	Sequence 5430, Ap
5	461.5	28.8	313	2	US-09-710-279-2568	Sequence 2568, Ap
6	461.5	28.8	317	2	US-09-134-001C-3366	Sequence 3366, Ap
7	460	28.7	243	2	US-09-134-000C-3753	Sequence 3753, Ap
8	254.5	15.9	306	2	US-09-489-039A-13474	Sequence 13474, A
9	219.5	13.7	315	2	US-09-252-991A-24352	Sequence 24352, A
10	211.5	13.2	320	2	US-09-543-681A-6146	Sequence 6146, Ap
11	198	12.3	281	2	US-09-902-540-11701	Sequence 11701, A
12	174.5	10.9	358	2	US-09-248-796A-15976	Sequence 15976, A
13	173.5	10.8	319	2	US-09-252-991A-30187	Sequence 30187, A
14	170	10.6	359	2	US-09-538-092-111	Sequence 111, App
15	158.5	9.9	300	2	US-09-710-279-1420	Sequence 1420, Ap
16	158.5	9.9	317	2	US-09-134-001C-4537	Sequence 4537, Ap

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1605	100.0	317	4	US-10-619-779-2	Sequence 2, Appli
2	461.5	28.8	313	5	US-10-793-626-2568	Sequence 2568, Ap
3	461.5	28.8	317	4	US-10-724-972A-4872	Sequence 4872, Ap
4	248	15.5	300	3	US-09-738-626-4711	Sequence 4711, Ap
5	248	15.5	300	6	US-11-055-822-536	Sequence 536, App
6	248	15.5	300	6	US-11-055-822-630	Sequence 630, App
7	243.5	15.2	323	4	US-10-156-761-9372	Sequence 9372, Ap
8	183	11.4	298	5	US-10-984-449-30	Sequence 30, Appl
9	171.5	10.7	318	6	US-11-079-463-5732	Sequence 5732, Ap
10	158.5	9.9	300	5	US-10-793-626-1420	Sequence 1420, Ap
11	158.5	9.9	317	4	US-10-724-972A-5107	Sequence 5107, Ap

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	501.5	31.2	311	6	US-10-471-571A-5274	Sequence 5274, Ap
2	203.5	12.7	286	6	US-10-471-571A-3792	Sequence 3792, Ap
3	111.5	6.9	385	7	US-11-056-355B-65027	Sequence 65027, A
4	111.5	6.9	422	7	US-11-056-355B-65026	Sequence 65026, A
5	110	6.9	379	7	US-11-056-355B-65028	Sequence 65028, A
6	109	6.8	570	7	US-11-330-403-15658	Sequence 15658, A
7	108.5	6.8	274	7	US-11-330-403-16533	Sequence 16533, A
8	103	6.4	567	7	US-11-330-403-12689	Sequence 12689, A
9	100	6.2	339	7	US-11-282-498-10	Sequence 10, Appl
10	99	6.2	573	7	US-11-330-403-12427	Sequence 12427, A
11	97.5	6.1	308	7	US-11-330-403-10558	Sequence 10558, A
12	97.5	6.1	308	7	US-11-330-403-16566	Sequence 16566, A
13	97	6.0	349	7	US-11-330-403-9576	Sequence

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	724	45.1	305	2	AC0828	probable oxidoredu
2	575.5	35.9	312	2	C86790	2-dehydropantoate
3	497.5	31.0	311	2	D90046	hypothetical prote
4	349.5	21.8	307	2	D97261	ketopantoate reduc
5	340.5	21.2	301	2	H71011	probable thiamin b
6	317.5	19.8	300	2	H75119	probable 2-dehydro
7	314	19.6	310	2	A70449	hypothetical prote
8	311.5	19.4	294	2	F69461	thiamin biosynthes
9	268.5	16.7	296	2	D82092	2-dehydropantoate
10	263	16.4	303	2	D84230	hypothetical prote
11	255.5	15.9	303	2	AC0385	2-dehydropantoate
12	248.5	15.5	337	2	T31129	hypothetical prote
13	242.5	15.1	323	2	T35004	probable oxidoredu
14	239.5	14.9	303	2	G90688	hypothetical prote
15	239.5	14.9	303	2	C85539	hypothetical prote
16	235.5	14.7	303	2	A64772	ketopantoate reduc

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	726	45.2	305	2	Q5PIJ0_SALPA	Q5pij0 salmonella
2	724	45.1	305	2	Q8Z4L0_SALTI	Q8z4l0 salmonella
3	723	45.0	305	2	Q8ZN23_SALTY	Q8zn23 salmonella
4	714	44.5	305	2	Q57LD8_SALCH	Q57ld8 salmonella
5	662	41.2	312	2	Q38ZN5_LACSS	Q38zn5 lactobacill
6	613.5	38.2	308	2	Q8XMA4_CLOPE	Q8xma4 clostridium
7	603	37.6	313	2	Q831Q5_ENTFA	Q831q5 enterococcu
8	593.5	37.0	312	2	Q3Y316_ENTFC	Q3y316 enterococcu
9	591.5	36.9	312	2	Q8KUB0_ENTFA	Q8kub0 enterococcu
10	575.5	35.9	312	1	PANE_LACLA	Q9cfy8 lactococcus
11	567.5	35.4	306	2	Q301F4_STRSU	Q301f4 streptococc
12	559	34.8	313	2	Q834J5_ENTFA	Q834j5 enterococcu
13	551	34.3	307	2	Q3CZI3_STRAG	Q3czi3 streptococc
14	551	34.3	307	2	Q3D6Z0_STRAG	Q3d6z0 streptococc
15	551	34.3	307	2	Q3DFS4_STRAG	Q3dfs4 streptococc
16	551	34.3	307	2	Q3DJ71_STRAG	Q3dj71 streptococc
17	551	34.3	307	2	Q3DV45_STRAG	Q3dv45 streptococc

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
- 5: gb_pr:*
- 6: gb_ro:*
- 7: gb_sts:*
- 8: gb_sy:*
- 9: gb_un:*
- 10: gb_vi:*
- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					ID	Description
	No.	Score	Query Match	Length	DB		
	1	954	100.0	954	2	CQ761047	CQ761047 Sequence
	2	785	82.3	785	2	CQ761057	CQ761057 Sequence
	3	198.8	20.8	110000	15	CR936503_00	CR936503 Lactobaci
	4	189.8	19.9	110000	15	BA000016_09	Continuation (10 o
	5	187.4	19.6	9749	2	BD193560	BD193560 Enterococ
c	6	187.4	19.6	110000	15	AE016830_04	Continuation (5 of
	7	187.4	19.6	110000	15	CP000026_03	Continuation (4 of
c	8	187.4	19.6	153571	15	AF454824	AF454824 Enterococ
	9	184.2	19.3	110000	15	AE014613_03	Continuation (4 of
c	10	184.2	19.3	145050	15	AL627275	AL627275 Salmonell
	11	182.8	19.2	110000	15	AE016830_23	Continuation (24 o
c	12	182.6	19.1	20897	15	AE008817	AE008817 Salmonell
c	13	182.6	19.1	110000	15	AE017220_27	Continuation (28 o
	14	173.4	18.2	939	2	CQ969768	CQ969768 Sequence
	15	173.4	18.2	981	2	AR347138	AR347138 Sequence
	16	168.2	17.6	906	2	CQ969438	CQ969438 Sequence

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	954	100.0	954	12	ADH01241	Adh01241	Alpha-ket
2	785	82.3	785	12	ADH01251	Adh01251	Alpha-ket
3	187.4	19.6	9749	2	AAX13091	Aax13091	Enterococ
4	187.4	19.6	9749	6	ABS98886	Abs98886	Enterococ
5	173.4	18.2	939	14	ADV16648	Adv16648	Enterococ
6	173.4	18.2	981	10	ADC92122	Adc92122	E. faeciu
7	168.2	17.6	906	14	ADV16318	Adv16318	E. faecal
8	167.4	17.5	2974	2	AAX13359	Aax13359	Enterococ

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	173.4	18.2	981	3	US-09-107-532A-1749	Sequence 1749, Ap
2	164.2	17.2	1038	3	US-09-134-000C-1283	Sequence 1283, Ap
3	154.4	16.2	840	3	US-09-134-000C-2025	Sequence 2025, Ap
4	152.4	16.0	960	3	US-09-107-532A-2561	Sequence 2561, Ap
5	150	15.7	732	3	US-09-134-000C-348	Sequence 348, App
6	135.6	14.2	3059	3	US-09-710-279-3651	Sequence 3651, Ap
7	135.2	14.2	9072	3	US-08-956-171E-45	Sequence 45, Appl
8	135.2	14.2	9072	3	US-08-781-986A-45	Sequence 45, Appl
9	133.8	14.0	942	3	US-09-710-279-2567	Sequence 2567, Ap
10	133.8	14.0	954	3	US-09-134-001C-529	Sequence 529, App
11	49	5.1	564	3	US-09-248-796A-3567	Sequence 3567, Ap
12	41.2	4.3	1200	3	US-09-248-796A-3981	Sequence 3981, Ap

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	954	100.0	954	8	US-10-619-779-1	Sequence 1, Appli
2	785	82.3	785	8	US-10-619-779-11	Sequence 11, Appl
3	187.4	19.6	9749	3	US-09-070-927A-154	Sequence 154, App
4	167.4	17.5	2974	3	US-09-070-927A-422	Sequence 422, App
5	135.6	14.2	3059	10	US-10-793-626-3651	Sequence 3651, Ap
6	135.2	14.2	9072	2	US-08-781-986A-45	Sequence 45, Appl
7	135.2	14.2	9072	8	US-10-329-624-45	Sequence 45, Appl
8	133.8	14.0	942	10	US-10-793-626-2567	Sequence 2567, Ap
9	133.8	14.0	954	8	US-10-724-972A-1100	Sequence 1100, Ap

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	153.6	16.1	924	9	US-11-348-413-7959	Sequence 7959, Ap
2	135.2	14.2	933	6	US-10-471-571A-5273	Sequence 5273, Ap
3	133.4	14.0	942	9	US-11-348-413-12700	Sequence 12700, A
4	132	13.8	924	9	US-11-348-413-733	Sequence 733, App
5	40.6	4.3	1323	6	US-10-471-571A-5587	Sequence 5587, Ap
6	38.2	4.0	1389	8	US-11-217-529-77691	Sequence 77691, A
7	37.4	3.9	2412	8	US-11-217-529-82371	Sequence 82371, A
8	37.2	3.9	770	6	US-10-449-902-15810	Sequence 15810, A
9	37.2	3.9	2576	6	US-10-449-902-14913	Sequence 14913, A
10	36.2	3.8	1137	9	US-11-348-413-1407	Sequence 1407, Ap
11	35.8	3.8	660	8	US-11-266-748A-300705	Sequence 300705,
c 12	35.8	3.8	100445	9	US-11-021-837-40	Sequence 40, Appl
13	35.6	3.7	1594	9	US-11-218-305-7873	Sequence 7873, Ap
14	35.6	3.7	1719	6	US-10-471-571A-5367	Sequence 5367, Ap
15	35.4	3.7	702	9	US-11-348-413-14067	Sequence 14067

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	44	4.6	586	13	CZ834246	CZ834246 OC__Ba021
	2	42	4.4	440	5	CJ346415	CJ346415 CJ346415
c	3	41.4	4.3	628	11	BH761007	BH761007 BMBAC318E
	4	41	4.3	424	13	CZ835756	CZ835756 OC__Ba021
c	5	40.8	4.3	868	14	CR168374	CR168374 Forward s
c	6	40.8	4.3	880	13	CZ958166	CZ958166 307672 To
	7	40.6	4.3	470	6	AY915772	AY915772 Schistoso
c	8	40.6	4.3	470	9	CX862203	CX862203 SJE_BC_C0
c	9	40.6	4.3	506	3	BU767728	BU767728 SJEBC05
c	10	40.4	4.2	582	3	BU877033	BU877033 V028F05 P
	11	40.4	4.2	626	11	AZ524120	AZ524120 227PbE08
c	12	40.4	4.2	851	13	DU038207	DU038207 21357 Tom
c	13	40.4	4.2	862	11	BH154498	BH154498 ENTRU94TR
c	14	40.4	4.2	879	11	AZ532665	AZ532665 ENTCTF30TF
	15	40.4	4.2	911	11	AZ530670	AZ530670 ENTCTF79TF